

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 11:03:09 ; Search time 3842.15 Seconds
(without alignments)
1807.663 Million cell updates/sec

Title: US-09-394-745-6489
Perfect score: 421
Sequence: 1 ggggccagcagcggtccggc.....ctcgacaagatctaaggggg 421

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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20: em_or:*
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26: em_sts:*
27: em_sy:*

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28: em_un:*
29: em_vi:*
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31: em_htgo_inv:*
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34: em_htg_inv:*
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36: em_htg_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query				Description
			No.	Score	Match	Length DB ID	
			1	212	50.4	163055 2	AP003626 Oryza sat
			2	212	50.4	165909 2	AP003711 Oryza sat
			3	96.4	22.9	1031 8	AF139499 Prunus ar
			4	91.8	21.8	105807 8	AC006085 Arabidops
			5	90.4	21.5	844 8	AF140722 Oryza sat
c			6	86.4	20.5	165873 2	AC090871 Oryza sat
c			7	84.4	20.0	136198 2	AP003883 Oryza sat
			8	81.6	19.4	871 8	PHVPVPR3A M75856 P.vulgaris
			9	79.6	18.9	165873 2	AC090871 Oryza sat
c			10	78.4	18.6	151085 8	AP003239 Oryza sat
			11	78.4	18.6	151100 8	AP003453 Oryza sat
c			12	78.4	18.6	159497 2	AP003288 Oryza sat
			13	72.6	17.2	871 8	AY042871 Arabidops
			14	72.6	17.2	100028 8	ATF3C22 AL353912 Arabidops
			15	69.2	16.4	21200 8	AP002044 Arabidops
c			16	69.2	16.4	105768 8	AC069474 Arabidops
c			17	67	15.9	118374 8	AC025416 Genomic s
			18	64.4	15.3	1382 9	BC011018 Homo sapi
			19	64.4	15.3	2273 9	AF062347 Homo sapi
			20	64.4	15.3	2347 9	AK025782 Homo sapi
			21	64.4	15.3	2418 9	AF062346 Homo sapi
			22	63.2	15.0	1621 3	AB001773 Ciona sav
			23	62.6	14.9	2167 10	AF062071 Mus muscu
			24	61.4	14.6	1279 8	AF361575 Arabidops
			25	61.4	14.6	2368 10	MMU251508 Mus muscu
			26	61.4	14.6	107600 8	ATF16J13 AL049638 Arabidops
			27	61.4	14.6	190026 8	ATCHRIV33 AL161533 Arabidops
			28	61	14.5	528 8	AF325093 Arabidops
			29	60.6	14.4	1197 6	AR044461 Sequence
			30	60.6	14.4	1451 9	HSA251095 Homo sapi
			31	60.6	14.4	1492 9	AF261138 Homo sapi
			32	60.6	14.4	1535 10	BC010683 Mus muscu
			33	60.6	14.4	1613 9	AF061739 Homo sapi
			34	60.6	14.4	1709 9	BC005283 Homo sapi
c			35	59.6	14.2	89350 8	ATT12H17 AL021635 Arabidops
c			36	59.6	14.2	139316 8	ATF7H19 AL031018 Arabidops
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			38	59	14.0	1512 6	AX086051 Sequence

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c	40	57.4	13.6	105689	8	AC005824	AC005824 Arabidops
	41	56.2	13.3	76042	8	AC006921	AC006921 Arabidops
	42	56.2	13.3	198944	8	ATCHRIV38	AL161538 Arabidops
	43	56.2	13.3	200576	8	ATFCA0	Z97335 Arabidopsis
	44	48.6	11.5	11019	9	AF062072	AF062072 Homo sapi
	45	48.6	11.5	162985	9	AL135924	AL135924 Human DNA

ALIGNMENTS

RESULT 1

AP003626

LOCUS AP003626 163055 bp DNA HTG 18-MAY-2001

DEFINITION Oryza sativa chromosome 6 clone P0429G06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.

ACCESSION AP003626

VERSION AP003626.1 GI:14141687

KEYWORDS HTG; HTGS_PHASE2.

SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:P0429G06.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (sites)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0429G06

JOURNAL Published Only in DataBase (2001) In press

REFERENCE 2 (bases 1 to 163055)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES

source

Location/Qualifiers

1. .163055

/organism="Oryza sativa"

/cultivar="Nipponbare"

/db_xref="taxon:4530"

/chromosome="6"

/clone="P0429G06"

BASE COUNT 47965 a 33832 c 33488 g 47470 t 300 others

ORIGIN

Query Match 50.4%; Score 212; DB 2; Length 163055;
Best Local Similarity 77.3%; Pred. No. 1.1e-38;
Matches 310; Conservative 0; Mismatches 81; Indels 10; Gaps 4;

Qy	19	gcaggatcaggccaagctggctgctcctctatcgacagcatcgtgaacggcagcgacgc	78
Db	122931	GCAGGAGCAGGCCAAGCTGGCAGCCTCCTCTATCGACAGCATTGTCAATGGTGGTGATTC	122990
Qy	79	cgtcatggagccggttgctggcagcaacacggtagtagctggtgcccaagttgagtt	138
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Qy	199	gatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagagggttg	258
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Qy	259	acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga	318
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Qy	319	caagcaocgactgcaagttcgactaacggactgctgccaaggacgccattgccaagggcta	378
Db	123222	TAAGCATGACTGCCAGTTTGACTATCGGACCGCTGCTAGGGATGCTATTGCCAA-GGCTA	123280
Qy	379	atccggtggtgaaggcagacaagctcgacaagatctaaggg	419
Db	123281	ATCCGGTGGTGAAGGCGGAGAACTTGACAAAATTTAGGGG	123321

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RESULT      2
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LOCUS       AP003711    165909 bp    DNA                HTG                31-MAY-2001
DEFINITION  Oryza sativa chromosome 6 clone P0417G12, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION   AP003711
VERSION     AP003711.1  GI:14270111
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Oryza sativa (cultivar:Nipponbare) DNA, clone:P0417G12.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (sites)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
            clone:P0417G12
  JOURNAL   Published Only in DataBase (2001) In press
REFERENCE   2  (bases 1 to 165909)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAY-2001) Takuji Sasaki, National Institute of

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Db	306	GCAATGGAAATGAACCTGTTGTTGCTGCTGGTGTGGATGTTCAAGCCCATCTGGTGGAGC	365
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Db	366	CAAAAACTATCTCTTTACAACCATCCTTTTCCTTTGGTTTCAGGTTTCAGGAGGGAGTGGTG	425
Qy	201	tctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttgac	260
Db	426	AGGCAAA-----GCCAGAAGGCCCAAAACGTTGCGGAAC TTGCAACAAGAGAGTTGGAT	479
Qy	261	ttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccgaca	320
Db	480	TAACAGGGTTCAATTGTCGGTGTGGTCACTTTTCTGTGCAGTACATCGTTATTTCAGACA	539
Qy	321	agcacgactgcaagttcgactaacggactgctgccaaaggacgccattgccaaagggcta	380
Db	540	AACATGACTGCCCTTATGATTACCACACTGCTGCACGCGATGTGATTGCTAA-AGCCAAC	598
Qy	381	ccggtggtgaaggcagacaagctcgacaagatctaag	417
Db	599	CCTGTTGTAAAGGCTGATAAGCTTGAAAAAATCTAAG	635

RESULT	4
AC006085	
LOCUS	AC006085 105807 bp DNA PLN 17-MAY-1999
DEFINITION	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.
ACCESSION	AC006085
VERSION	AC006085.1 GI:4165340
KEYWORDS	HTG.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 105807)
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 105807)
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
TITLE	Direct Submission
JOURNAL	Submitted (03-DEC-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE	3 (bases 1 to 105807)
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,

Lueros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
 Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-1999) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 REFERENCE 4 (bases 1 to 105807)
 AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
 Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
 Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
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 Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAY-1999) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT On Jan 21, 1999 this sequence version replaced gi:4079615.
 BAC F11M15 is near molecular marker m280 on Chromosome I.
 e-mail for correspondence: arab@sequence.stanford.edu
 Genes with similarity to proteins in the databases are described as
 'putative', '-like' or 'similar to'. Genes that have EST
 similarity but no significant protein similarity are described as
 'unknown proteins'. Genes that are annotated based only on gene
 prediction software are described as 'hypothetical proteins'.
 The software programs used to predict genes include: Grail
 (Informatics Group, Oak Ridge National Laboratory,
<http://compbio.ornl.gov/section/index.html>), GENSCAN (Chris Burge,
<http://gnomic.stanford.edu/~chris/GENSCANW.html>), Fexa (V.Solovyev
 & A.Salamov, Sanger Centre, <http://genomic.sanger.ac.uk/>), and
 NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark,<http://www.cbs.dtu.dk/NetPlantGene.html>).
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      QEQGAKFASAVSGTSSSSNIIKETFTAALVDIETKSVEPMTVSVQPSVQVVAEVVAP
      EEAAKPKGPSRCTTCNKRVGLTGFKRCGSLFCGTHRYADVHDCSFNYHAAAEQAIK
      ANPVVKAEKLDKI"
gene 40400. .41701

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Query Match 21.8%; Score 91.8; DB 8; Length 105807;
 Best Local Similarity 70.3%; Pred. No. 2.5e-11;
 Matches 137; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

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Qy 222 ggccgaaccggtgcagcgctgcaggaagagggttgacttacgggattcaactgccggt 281
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38609 GACCAAGCCGATGTACTACTTGAATAAGCGGGTTGGCCTGACTGGATTCAAATGTCGCT 38668

Qy 282 gtgggaacttgactgcgcaactccaccgctactccgacaagcacgactgcaagttcgact 341
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38669 GTGGGAGCCTCTTCTGCGGAACACACCGCTATGCAGACGTACATGACTGCTCCTTCAATT 38728

Qy 342 aacggactgctgccaaaggacgccattgccaaagggctaataccggtggtgaaggcagacaag 401
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 38729 ACCATGCTGCTGCGCAAGAGGCGATAGCTAA-GGCAAACCCGGTTGTGAAAGCAGAGAAG 38787

Qy 402 ctcgacaagatctaa 416
      | | | | | | | | | |
Db 38788 CTTGACAAAATCTGA 38802
  
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RESULT 5

AF140722

LOCUS AF140722 844 bp mRNA PLN 07-JUN-2000

DEFINITION Oryza sativa pathogenesis-related protein mRNA, complete cds.

ACCESSION AF140722

VERSION AF140722.1 GI:8307827

KEYWORDS .

SOURCE Oryza sativa.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 844)

AUTHORS Mukhopadhyay, A. and Tyagi, A.K.

TITLE Isolation and characterization of a novel pathogenesis-related
 protein gene (OSPR) from rice (Oryza sativa cv. Pusa Basmati 1)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 844)

AUTHORS Mukhopadhyay, A. and Tyagi, A.K.

TITLE Direct Submission

JOURNAL Submitted (06-APR-1999) Department of Plant Molecular Biology,
 University of Delhi, South Campus, Benito Juarez Road, New Delhi
 110021, India

FEATURES Location/Qualifiers

source 1..844

/organism="Oryza sativa"

/cultivar="Pusa Basmati 1"

/db_xref="taxon:4530"

CDS 110..604

/note="OSPR"

/codon_start=1

/product="pathogenesis-related protein"

/protein_id="AAF74344.1"

/db_xref="GI:8307828"

/translation="MAQRDKKDQEPTELRAPEITLCANSCGFPGNPATQNLQCNCFLA
 ATASTSSPSSLSSPVLDKQPPRPAAPLVEPQAPLPPPVEEMASALATAPAPVAKTSAV"

NRCSRCRKRVGLTGFRRCRGLFCGEHRYSDRHGCSYDYKSAARDAIARDNPVVRAAK
IVRF"

BASE COUNT 206 a 225 c 249 g 164 t
ORIGIN

Query Match 21.5%; Score 90.4; DB 8; Length 844;
Best Local Similarity 64.4%; Pred. No. 1e-10;
Matches 150; Conservative 0; Mismatches 82; Indels 1; Gaps 1;

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Qy 188 ggggtggcgcgatctccaaagggggaagggtanggccgaaccggtgcagcgctgcagg 247
    | | ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 377 GCGACGGCGCCGGCGCCGGTTCGCCAAGACGTCGGCGGTGAACCGGTGCTCCAGGTGCCGG 436

Qy 248 aagaggggttgacttacgggattcaactgccggtgtgggaacttgtactgcgcactccac 307
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 437 AAGCGTGTTCGGCCTCACCGGGTTCGGGTGCCGGTGCGGCCACCTGTTCTGCGGCGAACAC 496

Qy 308 cgctactccgacaagcagcactgcaagttcgactaacggactgctgccaaggacgccatt 367
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 497 CGGTACTCCGACCGCCACGGCTGCAGCTACGACTACAAGTCGGCGGCAAGGGACGCCATC 556

Qy 368 gccaaagggctaataccggtggtgaaggcagacaagctcgacaagatctaagggg 420
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 557 GCC-AGGGACAACCCGGTGGTGC GCGCGGCCAAGATCGTTAGGTTCTGAGAGG 608
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RESULT 6
AC090871/c
LOCUS AC090871 165873 bp DNA HTG 28-JUN-2001
DEFINITION Oryza sativa chromosome 3 clone OSJNBb0060J21, *** SEQUENCING IN
PROGRESS ***, 5 unordered pieces.
ACCESSION AC090871
VERSION AC090871.7 GI:14573697
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 165873)
AUTHORS Buell,R., Hsiao,J., Zismann,V., Moffat,K.M., Hill,J.,
Gansberger,K., Burgess,S., Jarrahi,B., Shvartsbeyn,M., Brenner,M.,
Ciecko,A., Pai,G., Vanaken,S., Hansen,C., Utterbach,T.,
Feldblyum,T., Khalak,H.G., Yuan,Q., Quackenbush,J., White,O.,
Salzberg,S. and Fraser,C.
TITLE Oryza sativa ssp. japonica cv. Nipponbare OSJNBb0060J21 BAC genomic
sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165873)
AUTHORS Buell,R.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
COMMENT On Jun 28, 2001 this sequence version replaced gi:14333942.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 11885: contig of 11885 bp in length
 * 11886 11923: gap of unknown length
 * 11924 28536: contig of 16613 bp in length
 * 28537 28574: gap of unknown length
 * 28575 95942: contig of 67368 bp in length
 * 95943 95979: gap of unknown length
 * 95980 122498: contig of 26519 bp in length
 * 122499 122535: gap of unknown length
 * 122536 165873: contig of 43338 bp in length.

FEATURES Location/Qualifiers
 source 1. .165873
 /organism="Oryza sativa"
 /cultivar="Nipponbare"
 /sub_species="japonica"
 /db_xref="taxon:4530"
 /chromosome="3"
 /clone="OSJNBb0060J21"
 BASE COUNT 46732 a 35660 c 36160 g 47138 t 183 others
 ORIGIN

Query Match 20.5%; Score 86.4; DB 2; Length 165873;
 Best Local Similarity 65.7%; Pred. No. 4e-10;
 Matches 140; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

Qy 195 cggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgctgcaggaagaggg 254
 || || | | |||| | || | |||| |||| | || || || || ||
 Db 33044 CGTCGCCGGCGACGGGGGAGCAGCCGGAGGCGAACC GGTCGCGACGTGCCGGAGGAAGG 32985
 Qy 255 ttggacttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctact 314
 | || || |||| |||| |||| || || | || |||| |||| ||||
 Db 32984 TGGGGCTGACGGGGTTCAAGTGCCGGTGCGGCGGCACGTTCTGCGGCGGCCACCGCTACG 32925
 Qy 315 ccgacaagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagg 374
 |||| |||| |||| |||| |||| || || | | || || || || ||
 Db 32924 CCGACGAGCACGGCTGCGGCTTCGACTACAAGAGCTCCGGGAGGGAGCTGATCGCCAA-G 32866
 Qy 375 gctaataccggtggtgaaggcagacaagctcgac 407
 |||| || || || || || || || || || || || || || || ||
 Db 32865 CAGAATCCGGTCGTCGTCGCCGACAAGCTGGCC 32833

RESULT 7
 AP003883/c
 LOCUS AP003883 136198 bp DNA HTG 10-JUL-2001
 DEFINITION Oryza sativa chromosome 8 clone OJ1134_H03, *** SEQUENCING IN
 PROGRESS ***, in ordered pieces.
 ACCESSION AP003883
 VERSION AP003883.1 GI:14646816
 KEYWORDS HTG; HTGS_PHASE2.
 SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1134_H03.

| | | | | | | |
Db 87039 TAGGTTCTAAAAGG 87026

RESULT 8

PHVPVPR3A

LOCUS PHVPVPR3A 871 bp mRNA PLN 12-AUG-1994

DEFINITION P.vulgaris PVPR3 protein mRNA, complete cds.

ACCESSION M75856

VERSION M75856.1 GI:169362

KEYWORDS PVPR3 protein.

SOURCE Phaseolus vulgaris cDNA to mRNA.

ORGANISM Phaseolus vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.

REFERENCE 1 (bases 1 to 871)

AUTHORS Sharma,Y.K., Hinojos,C.M. and Mehdy,M.

TITLE cDNA cloning, structure and expression of a novel pathogenesis
related protein in bean

JOURNAL Mol. Plant Microb. Interact. 5, 89-95 (1992)

FEATURES Location/Qualifiers

source 1. .871

/organism="Phaseolus vulgaris"

/db_xref="taxon:3885"

mRNA 1. .871

/gene="PVPR3"

gene 1. .871

/gene="PVPR3"

CDS 116. .529

/gene="PVPR3"

/codon_start=1

/protein_id="AAA33773.1"

/db_xref="GI:169363"

/translation="MAQKAQKNDTDFKVPEPITPCATATAAAATSISEPSRFFDAATP

ATSSRSPKRSLEDAANADRTVASEPKRAVNRCSGCRRRVGLTGFRRCRGLFCAEH

RYTDRHDCSYDYKTVGREAIARENPVVKAIVKV"

primer_bind complement(195. .212)

/gene="PVPR3"

/note="5' primer"

BASE COUNT 209 a 234 c 198 g 230 t

ORIGIN

Query Match 19.4%; Score 81.6; DB 8; Length 871;

Best Local Similarity 63.3%; Pred. No. 1e-08;

Matches 140; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

Qy 196 ggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgctgcaggaagagggt 255

Db 310 GACGGTGGCATCGGAGCCGAAGCGCGCGGTGAACCGGTGCTCGGGATGCCGGCGGCGCGT 369

Qy 256 tggacttacgggattcaactgccggtgtgggaacttgtagctgcgcactccaccgctactc 315

Db 370 CGGGCTGACCGGATTCCGCTGTGCGGTGCGGTGACCTTTTCTGCGCTGAGCACCGGTACAC 429

Qy 316 cgacaagcacgactgcaagttcgactaacggactgctgccaggacgccattgccaaggg 375
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 Db 430 GGACCGCCACGACTGCTCCTACGACTACAAGACCGTCGGGAGAGAGGCCATCG-CGAGGG 488

Qy 376 ctaatccggtggtgaaggcagacaagctcgacaagatctaa 416
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 Db 489 AGAATCCCGTCGTGAAGGCCGCGAAGATCGTGAAGGTCTGA 529

RESULT 9

AC090871

LOCUS AC090871 165873 bp DNA HTG 28-JUN-2001

DEFINITION Oryza sativa chromosome 3 clone OSJNBb0060J21, *** SEQUENCING IN
 PROGRESS ***, 5 unordered pieces.

ACCESSION AC090871

VERSION AC090871.7 GI:14573697

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Oryza sativa.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 165873)

AUTHORS Buell,R., Hsiao,J., Zismann,V., Moffat,K.M., Hill,J.,
 Gansberger,K., Burgess,S., Jarrahi,B., Shvartsbeyn,M., Brenner,M.,
 Ciecko,A., Pai,G., Vanaken,S., Hansen,C., Utterbach,T.,
 Feldblyum,T., Khalak,H.G., Yuan,Q., Quackenbush,J., White,O.,
 Salzberg,S. and Fraser,C.

TITLE Oryza sativa ssp. japonica cv. Nipponbare OSJNBb0060J21 BAC genomic
 sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 165873)

AUTHORS Buell,R.

TITLE Direct Submission

JOURNAL Submitted (13-MAR-2001) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA

COMMENT On Jun 28, 2001 this sequence version replaced gi:14333942.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 11885: contig of 11885 bp in length
 * 11886 11923: gap of unknown length
 * 11924 28536: contig of 16613 bp in length
 * 28537 28574: gap of unknown length
 * 28575 95942: contig of 67368 bp in length
 * 95943 95979: gap of unknown length
 * 95980 122498: contig of 26519 bp in length
 * 122499 122535: gap of unknown length
 * 122536 165873: contig of 43338 bp in length.

FEATURES Location/Qualifiers

source 1. .165873

/organism="Oryza sativa"

/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="3"
/clone="OSJNBb0060J21"

BASE COUNT 46732 a 35660 c 36160 g 47138 t 183 others
ORIGIN

Query Match 18.9%; Score 79.6; DB 2; Length 165873;
Best Local Similarity 67.7%; Pred. No. 1.4e-08;
Matches 126; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

Qy 223 gccgaaccggtgcagcgccctgcaggaagaggggttgacttacgggattcaactgccggtg 282
||||||| || ||| ||||| ||| || ||||| ||||| |||||
Db 123242 GCCGAACCGGTGCGCGGCGTGCCGGAAGAAGGTGGGGCTGACGGGGTTCAAGTGCCGGTG 123301

Qy 283 tgggaacttgctactgcgcactccaccgctactccgacaagcacgactgcaagttcgacta 342
|| | ||| | ||||| || ||||| ||||| ||||| |||||
Db 123302 CGGCGGCAACTTCTGTGGCGGCCACCGCCACGCCGACGCCACGGCTGCGGCTTCGACTA 123361

Qy 343 acggactgctgccaaggacgccattgccaaagggttaacccggtggtgaaggcagacaagc 402
|| ||| ||||| || ||||| | || ||| || || |||||
Db 123362 CAAGAGCGCCGGAAGGAGCAGATCGCCAA-GCAGAACCCGCTCGTCGTCGCCGACAAGC 123420

Qy 403 tcgaca 408
| | |
Db 123421 TGGCCA 123426

RESULT 10

AP003239/c

LOCUS AP003239 151085 bp DNA PLN 07-MAR-2001

DEFINITION Oryza sativa genomic DNA, chromosome 1, PAC clone:P0403C05,
complete sequence.

ACCESSION AP003239

VERSION AP003239.2 GI:13365491

KEYWORDS HTG.

SOURCE Oryza sativa (cultivar:Nipponbare) DNA, clone:P0403C05.

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (sites)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0403C05

JOURNAL Published Only in DataBase (2001) In press

REFERENCE 2 (bases 1 to 151085)

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Direct Submission

JOURNAL Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT On Mar 16, 2001 this sequence version replaced gi:13027269.

COMMENT On Aug 9, 2001 this sequence version replaced gi:13486922.
The orientation of the sequence is from T7 to SP6 of the PAC clone.

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BASE COUNT      42198 a   33215 c   33471 g   42216 t
ORIGIN

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Qy 392 ggcagacaagctcgacaagatctaa 416
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 Db 108983 ACCCGACAAGGTGGAGAAGCTCTGA 109007

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RESULT 12
AP003288/c
LOCUS      AP003288    159497 bp    DNA                HTG                21-FEB-2001
DEFINITION Oryza sativa chromosome 1 clone P0683B11, *** SEQUENCING IN
            PROGRESS ***, in ordered pieces.
ACCESSION  AP003288
VERSION    AP003288.1  GI:13027318
KEYWORDS   HTG; HTGS_PHASE2.
SOURCE     Oryza sativa (cultivar:Nipponbare) DNA, clone:P0683B11.
            ORGANISM   Oryza sativa
                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                        Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1  (sites)
            AUTHORS    Sasaki,T., Matsumoto,T. and Yamamoto,K.
            TITLE      Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                        clone:P0683B11
            JOURNAL     Published Only in DataBase (2001) In press
REFERENCE  2  (bases 1 to 159497)
            AUTHORS    Sasaki,T., Matsumoto,T. and Yamamoto,K.
            TITLE      Direct Submission

```

```

JOURNAL      Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
              Agrobiological Resources, Rice Genome Research Program; Kannondai
              2-1-2, Tsukuba, Ibaraki 305-8602, Japan
              (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
              Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT      NOTE: It currently consists of 1 contigs. Gaps between the contigs
              are represented as runs of N. The order of the pieces is believed
              to be correct as given, however the sizes of the gaps between them
              are based on estimates that have provided by the submitter. This
              sequence will be replaced by the finished sequence as soon as it is
              available and the accession number will be preserved.
              * NOTE: This is a 'working draft' sequence.
              * This sequence will be replaced
              * by the finished sequence as soon as it is available and
              * the accession number will be preserved.

FEATURES             Location/Qualifiers
     source            1. .159497
                      /organism="Oryza sativa"
                      /cultivar="Nipponbare"
                      /db_xref="taxon:4530"
                      /chromosome="1"
                      /clone="P0683B11"

BASE COUNT      45304 a  34607 c  35698 g  43688 t      200 others
ORIGIN

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RESULT 13
AY042871
LOCUS      AY042871      871 bp      mRNA      PLN      04-JUL-2001
DEFINITION Arabidopsis thaliana zinc finger-like protein (F3C22_200) mRNA,
            complete cds.
ACCESSION  AY042871
VERSION    AY042871.1  GI:14596166
KEYWORDS   FLI_CDNA.
SOURCE     thale cress.
            ORGANISM  Arabidopsis thaliana

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 871)

AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

FEATURES Location/Qualifiers

source 1. .871
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="III"
/clone="RAFL04-17-A20"
/note="This clone is in pBluescript ecotype: Columbia"

gene 1. .871
/gene="F3C22_200"

CDS 93. .602
/gene="F3C22_200"
/codon_start=1
/product="zinc finger-like protein"
/protein_id="AAK68811.1"
/db_xref="GI:14596167"
/translation="MAEEHRCQTPESNRLCVNCGFLGSATMNLCSNCYGDLCLKQQQ
QSSSIKSTVESSLVSPSSSSSEISSPIIPLLKNPSVKLEVPEKKAVISLPTEQN
QQQRPNRCTTCRKRVLGTGFKCRCGTMFCGVHRYPEIHGCSYDFKSAGREEIAKANPL
VKA AKLQKI"

BASE COUNT 216 a 208 c 190 g 257 t

ORIGIN

Query Match 17.2%; Score 72.6; DB 8; Length 871;

Best Local Similarity 64.1%; Pred. No. 1.1e-06;
Matches 125; Conservative 0; Mismatches 69; Indels 1; Gaps 1;

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Qy 222 ggccgaaccggtgcagcgcctgcaggaagagggttgacttacgggattcaactgccggt 281
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Db 409 GGCCGAATCGGTGCACGACGTGTAGGAAACGGTCGGGTTAACCGGATTCAAGTGCCGGT 468

Qy 282 gtgggaacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgact 341
    ||| | ||| |||| | || | ||| | || | ||| | ||| |
Db 469 GCGGTACGATGTTTTGCGGGGTTTCATAGGTACCCGGAGATCCATGGATGCAGCTACGATT 528

Qy 342 aacggactgctgccaaaggacgccattgccaaagggttaatccggtggtgaaggcagacaag 401
    | || | || | || || | || ||||| ||||| |||| |
Db 529 TCAAATCGCCGGACGTGAAGAGATCGCGAA-AGCGAATCCGTTGGTGAAAGCAGCGAAG 587

Qy 402 ctcgacaagatctaa 416
    || | |||| | |
Db 588 CTTCAGAAGATATGA 602
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RESULT 14

ATF3C22

LOCUS ATF3C22 100028 bp DNA PLN 27-APR-2000

DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone F3C22.

ACCESSION AL353912

VERSION AL353912.1 GI:7669934

KEYWORDS .

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 100028)

AUTHORS Purnelle,B., Masuy,D., Goffeau,A., Boutry,M., Mewes,H.W., Rudd,S.,
Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 100028)

AUTHORS EU Arabidopsis sequencing,project.

TITLE Direct Submission

JOURNAL Submitted (27-APR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
Gaston Cremieux, BP191, 91006 Evry Cedex, France;
<http://www.genoscope.cns.fr>

COMMENT Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

FEATURES Location/Qualifiers

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/variety="Columbia"

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/chromosome="3"

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1. .31726

/note="overlap to BAC F2206, EMBL:AL050300; please refre

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RESULT 15

AP002044

LOCUS AP002044 21200 bp DNA PLN 19-JUL-2000

DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMF12.

ACCESSION AP002044

VERSION AP002044.1 GI:8051652

KEYWORDS .

SOURCE Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1 clone:MMF12.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (sites)

AUTHORS Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.
 TITLE Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC and BAC clones

JOURNAL DNA Res. 7 (3), 217-221 (2000)

MEDLINE 20363099

REFERENCE 2 (bases 1 to 21200)

AUTHORS Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
 TITLE Direct Submission

JOURNAL Submitted (16-MAY-2000) to the DDBJ/EMBL/GenBank databases.
 Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

COMMENT Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MMF12

Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail

(Informatics Group, Oak Ridge National Laboratory,

<http://compbio.ornl.gov/Grail-1.3/>),

GENSCAN (Chris Burge, MIT, <http://CCR-081.mit.edu/GENSCAN.html>),

NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/services/NetGene2/>) and

SplicePredictor (Volker Brendel, Stanford University,

http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SE
 (Sean Eddy, Washington University School of Medicine, St. Louis,
 http://genome.wustl.edu/eddy/tRNAscan-SE/).
 This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is T16H11 and the 3' clone is MBK21.

FEATURES	Location/Qualifiers
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Matches 121; Conservative 0; Mismatches 68; Indels 1; Gaps 1;

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Qy 347 actgctgccaaggagcgccattgccaaagggttaatccgggtggtgaaggcagacaagctcga 406
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Qy 407 caagatctaa 416
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Db 19291 CAAAGTTTAA 19300

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Job time: 9912 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 11:00:01 ; Search time 428.31 Seconds
 (without alignments)
 842.693 Million cell updates/sec

Title: US-09-394-745-6489
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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
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	2	93	22.1	1116	21	AAC52046	Arabidopsis thalia
	3	91.8	21.8	522	21	AAC43443	Arabidopsis thalia
	4	91.8	21.8	928	21	AAC49898	Arabidopsis thalia
	5	91.8	21.8	986	21	AAC49893	Arabidopsis thalia
	6	81.4	19.3	941	21	AAC40316	Arabidopsis thalia
	7	72.6	17.2	819	21	AAC47807	Arabidopsis thalia
	8	72.6	17.2	896	21	AAC37805	Arabidopsis thalia
	9	72.6	17.2	1155	21	AAC36681	Arabidopsis thalia
	10	71	16.9	1028	21	AAC37406	Arabidopsis thalia
	11	69.2	16.4	830	21	AAC35523	Arabidopsis thalia
	12	68	16.2	348	21	AAC57020	Pinus radiata tran
	13	67	15.9	862	21	AAC40557	Arabidopsis thalia
	14	66.8	15.9	594	21	AAC41669	Arabidopsis thalia
	15	64.4	15.3	1425	22	AAH22181	Human zinc finger
	16	64.4	15.3	2487	21	AAF15969	Human prostate can
	17	62.6	14.9	2517	20	AAZ28269	Rat neuronal immed
	18	61.4	14.6	890	21	AAC47427	Arabidopsis thalia
	19	60.6	14.4	1197	19	AAV61061	Human ubiquitin co
	20	60.6	14.4	1197	20	AAX78444	Human UCSP-2 cDNA.
	21	60.6	14.4	1200	21	AAA39269	cDNA encoding huma
	22	60.6	14.4	1251	22	AAH22180	Human zinc finger
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	24	59.6	14.2	855	21	AAC46325	Arabidopsis thalia
	25	59	14.0	1599	22	AAI57828	Human polynucleoti
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	27	58	13.8	857	21	AAC35304	Arabidopsis thalia
	28	57.4	13.6	831	21	AAC50001	Arabidopsis thalia
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	36	53.6	12.7	329	21	AAC56980	Pinus radiata tran
	37	48.6	11.5	594	22	AAI41946	Probe #10632 used
	38	45.2	10.7	149	22	AAI54980	Probe #23666 used
	39	44	10.5	378	14	AAQ60725	Human brain Expres
	40	43	10.2	535	22	AAI17609	Probe #7542 for ge
	41	43	10.2	535	22	AAI42527	Probe #11213 used
	42	41.6	9.9	181	21	AAC05414	Human secreted pro
	43	41.6	9.9	183	20	AAX51534	Human secreted pro
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 DT 17-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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PN EP1033405-A2.
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DT 18-OCT-2000 (first entry)

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KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.
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Qy	282	gtgggaacttgtactgcgcactccaccgctactccgacaagcacgactgcaagttcgact	341
Db	389	gtgggagcctcttctgcggaacacaccgctatgcagacgtacatgactgctccttcaatt	448
Qy	342	aacggactgctgccaaaggacgccattgccaagggctaataccgggtggtgaaggcagacaag	401
Db	449	accatgctgctgcgcaagaggcgatagctaa-ggcaaaccgggttgtgaaagcagagaag	507
Qy	402	ctcgacaagatctaa	416
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DT    18-OCT-2000   (first entry)
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KW    Hybridisation assay; genetic mapping; gene expression control;
KW    protein identification; signal transduction pathway;
KW    metabolic pathway; promoter; termination sequence; ss.
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OS    Arabidopsis thaliana.
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PN    EP1033405-A2.
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KW    metabolic pathway; promoter; termination sequence; ss.
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DT 18-OCT-2000 (first entry)

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DT 17-OCT-2000 (first entry)

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PN EP1033405-A2.

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PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
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PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
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 Db 683 ggccgaatcggtgcacgacgtgtaggaaacgggtcggttaaccggattcaagtgccggt 742

Qy 282 gtgggaacttgactgcgccactccaccgctactccgacaagcacgactgcaagttcgact 341
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 Db 743 gcggtacgatgttttgcgggggttcattaggtaccgagatccatggatgcagctacgatt 802

Qy 342 aacggactgctgccaaaggacgccattgccaaagggttaattccggtggtgaaggcagacaag 401
 | | | | | | | | | | | | | | | | | | | | | |
 Db 803 tcaaatcgccggacgtgaagagatcgcgaa-agcgaatccgttggtgaaagcagcgaag 861

Qy 402 ctcgacaagatctaa 416
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 Db 862 cttcagaagatatga 876

RESULT 10

AAC37406

ID AAC37406 standard; DNA; 1028 BP.

XX

AC AAC37406;

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DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 17264.

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KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

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PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

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PR 16-APR-1999; 99US-0129845.

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PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

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PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

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PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
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PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
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PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.

PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
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 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
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 PR 14-OCT-1999; 99US-0159638.
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Query Match 16.9%; Score 71; DB 21; Length 1028;
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 Qy 282 gtgggaacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgact 341
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 Db 521 tcggtacgatgttttgcgggggttcataaggtaccggagatccatggatgcagctacgatt 580

Qy 342 aacggactgctgccaaggacgccattgccaaagggctaataccggtggtgaaggcagacaag 401
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 Db 581 tcaaatacgccggacgtgaagagatcgcgaa-agcgaatccggtggtgaaagcagcgaag 639
 Qy 402 ctcgacaagatctaa 416
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 Db 640 cttcagaagatatga 654

RESULT 11

AAC35523

ID AAC35523 standard; DNA; 830 BP.

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AC AAC35523;

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DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 10502.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

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PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

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PR	18-JUN-1999;	99US-0139456.
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PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
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PR	06-AUG-1999;	99US-0147303.
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PR	09-AUG-1999;	99US-0147493.
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PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
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PR	16-AUG-1999;	99US-0149368.
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PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
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PR	31-AUG-1999;	99US-0151438.
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PR 20-SEP-1999; 99US-0154779.
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 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

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 Best Local Similarity 63.7%; Pred. No. 1.4e-09;
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 Qy 347 actgctgccaaaggacgccattgccaaagggttaatccggtggtgaaggcagacaagctcga 406
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Qy 407 caagatctaa.416
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Db 573 caaagtttaa 582

RESULT 12

AAC57020

ID AAC57020 standard; DNA; 348 BP.

XX

AC AAC57020;

XX

DT 25-JAN-2001 (first entry)

XX

DE Pinus radiata transcription factor DNA sequence #466.

XX

KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB; ss.

XX

OS Pinus radiata.

XX

PN WO200053724-A2.

XX

PD 14-SEP-2000.

XX

PF 09-MAR-2000; 2000WO-US06112.

XX

PR 11-MAR-1999; 99US-0266513.

PR 18-AUG-1999; 99US-0149485.

XX

PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX

PI Wood M, McGrath A, Shenk MA, Glenn M;

XX

DR WPI; 2000-579369/54.

XX

PT New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
PT -

XX

PS Claim 1; Pages 567-568; 747pp; English.

XX

CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members from the
CC following families of regulatory proteins: bZIP, bZIP family of G-box
CC binding factors, basic helix-loop-helix zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements

CC and MYB.
XX
SQ Sequence 348 BP; 81 A; 92 C; 107 G; 68 T; 0 other;

Query Match 16.2%; Score 68; DB 21; Length 348;
Best Local Similarity 63.0%; Pred. No. 2.4e-09;
Matches 104; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

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Qy 267 gattcaactgccggtgtgggaacttgactgcgcactccaccgctactccgacaagcacg 326
    | || | |||| |||| || | |||| | || | |||| || | |||
Db 244 gctttaagtgccgctgtggtgaccttttctgcgctcagcacaggtactctgatatgcatg 303

Qy 327 actgcaagttcgactaacggactgctgccaaggacgccattgcc 371
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Db 304 actgctcttttgactacaagactgccggcgctcgccatttctca 348
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RESULT 13

AAC40557

ID AAC40557 standard; DNA; 862 BP.

XX

AC AAC40557;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 28736.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

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PR 06-APR-1999; 99US-0128234.

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PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

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 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
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 PR 04-OCT-1999; 99US-0157117.
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 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 15.9%; Score 67; DB 21; Length 862;
 Best Local Similarity 62.8%; Pred. No. 5.7e-09;
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Qy 231 ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact 290
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Db 476 gatgcttgagctgtaacaagaaagttggcgtgacgggtttcaagtgtaggtgtggaagca 535

Qy 291 tgtactgcgcactccaccgctactccgacaagcagactgcaagttcgactaacggactg 350
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RESULT 14

AAC41669

ID AAC41669 standard; DNA; 594 BP.

XX

AC AAC41669;

XX

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 32705.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

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PR 30-APR-1999; 99US-0132407.

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PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
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PR	28-JUL-1999;	99US-0145951.
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PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
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PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
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PR	12-AUG-1999;	99US-0148341.
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PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
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 PR 22-SEP-1999; 99US-0155139.
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 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
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 PR 14-OCT-1999; 99US-0159637.
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 PR 21-OCT-1999; 99US-0160741.
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 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
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 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

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Qy 291 tgtactgcgactccaccgctactccgacaagcacgactgcaagttcgactaacggactg 350
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 Db 470 ctttctgtggaactcatagatatccagagagtcacgagtgccaattcgatttcaaaggag 529

Qy 351 ctgccaaggacgccattgccaaagggctaatccggtggtgaaggcagacaagctcgacaag 410
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Qy 411 atctaa 416
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 Db 589 atatga 594

RESULT 15

AAH22181

ID AAH22181 standard; cDNA; 1425 BP.

XX

AC AAH22181;

XX

DT 20-AUG-2001 (first entry)

XX

DE Human zinc finger protein (hZNF216) nucleotide sequence.

XX

KW Human; hZNF216-iso; hZNF216; zinc finger protein; ss.

XX

OS Homo sapiens.

XX

PN CN1281898-A.

XX

PD 31-JAN-2001.

XX

PF 27-JUN-2000; 2000CN-0116798.

XX

PR 27-JUN-2000; 2000CN-0116798.

XX

PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.

XX

PI Li N, Xu X, Xiao H;

XX

DR WPI; 2001-282784/30.

DR P-PSDB; AAB98228.

XX

PT New human zinc finger protein isomer, hZNF216, polypeptide and
 PT polynucleotide useful for detecting hZNF216 -

XX

PS Example 2; Fig 2; 23pp; Chinese.

XX

CC The present invention describes a human zinc finger protein isomer,
 CC designated hZNF216-iso. Also described are methods for the preparation
 CC and detection of hZNF216-iso protein and nucleotide sequences. The
 CC present sequence represents the human zinc finger protein hZNF216
 CC nucleotide sequence which is given in comparison with the hZNF216-iso
 CC nucleotide sequence in an example from the present invention.

XX

SQ Sequence 1425 BP; 464 A; 279 C; 300 G; 382 T; 0 other;

Query Match 15.3%; Score 64.4; DB 22; Length 1425;
Best Local Similarity 62.1%; Pred. No. 3.3e-08;
Matches 118; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

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Db 492 aacagatgtttcatgtgcagaaagaaagttggtcttacagggttgactgccgatgtgga 551

Qy 287 aacttgactgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacgg 346
    || |||| || | |||| |||| |||| |||| |||| || || ||
Db 552 aatttgttttgtggacttcaccgttactctgacaagcacaactgtccgtatgattacaaa 611

Qy 347 actgctgccaaggacgccattgccaaagggttaatccggtggtgaaggcagacaagctcga 406
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Qy 407 caagatctaa 416
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Db 671 gagaatataa 680
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Search completed: February 7, 2002, 11:00:03
Job time: 4989 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 10:51:52 ; Search time 172.96 Seconds
(without alignments)
551.268 Million cell updates/sec

Title: US-09-394-745-6489
Perfect score: 421
Sequence: 1 ggggccagcacgcgtccggc.....ctcgacaagatctaaggggg 421

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	60.6	14.4	1197	1	US-08-861-269-4			Sequence 4, Appli
	2	60.6	14.4	1197	2	US-09-134-596-4			Sequence 4, Appli
	3	60.6	14.4	1197	3	US-09-293-273-4			Sequence 4, Appli
c	4	35.8	8.5	7218	1	US-08-232-463-14			Sequence 14, Appl
	5	35.4	8.4	4411529	4	US-09-103-840A-1			Sequence 1, Appli
	6	34.6	8.2	459	2	US-08-387-942C-37			Sequence 37, Appl
	7	34.6	8.2	12588	2	US-08-387-942C-1			Sequence 1, Appli
	8	34.4	8.2	750	3	US-09-167-717-3			Sequence 3, Appli
	9	33.2	7.9	80161	3	US-09-036-987A-1			Sequence 1, Appli
	10	33.2	7.9	80161	4	US-09-370-700-1			Sequence 1, Appli
	11	33.2	7.9	4403765	4	US-09-103-840A-2			Sequence 2, Appli
	12	33	7.8	2899	4	US-08-981-392-24			Sequence 24, Appl
	13	32.4	7.7	4601	1	US-08-470-058-3			Sequence 3, Appli
	14	32.4	7.7	4601	3	US-09-037-188-3			Sequence 3, Appli
	15	32.4	7.7	4601	4	US-09-285-310-3			Sequence 3, Appli
	16	32.4	7.7	5095	1	US-08-092-817-3			Sequence 3, Appli
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c	19	32.2	7.6	4983	1	US-08-472-358-1			Sequence 1, Appli
c	20	32.2	7.6	4983	5	PCT-US92-05786A-1			Sequence 1, Appli
c	21	31.8	7.6	2015	1	US-07-937-609-25			Sequence 25, Appl
c	22	31.8	7.6	2015	4	US-08-029-170-25			Sequence 25, Appl
c	23	31.6	7.5	1950	3	US-08-911-853-14			Sequence 14, Appl
c	24	31.6	7.5	1950	4	US-09-479-409-14			Sequence 14, Appl
	25	31.6	7.5	5247	1	US-08-920-812-15			Sequence 15, Appl
	26	31.6	7.5	5247	1	US-08-920-827-15			Sequence 15, Appl
	27	31.6	7.5	5247	1	US-08-921-177-15			Sequence 15, Appl
	28	31.6	7.5	5247	1	US-08-362-577C-15			Sequence 15, Appl
	29	31.6	7.5	5247	2	US-08-920-828-15			Sequence 15, Appl
	30	31.6	7.5	17612	3	US-08-911-853-29			Sequence 29, Appl
	31	31.6	7.5	17612	4	US-09-479-409-29			Sequence 29, Appl
c	32	31.6	7.5	4403765	4	US-09-103-840A-2			Sequence 2, Appli
c	33	31	7.4	1195	1	US-08-117-373-5			Sequence 5, Appli
c	34	31	7.4	3914	1	US-08-117-373-11			Sequence 11, Appl
	35	31	7.4	11220	4	US-09-105-537-32			Sequence 32, Appl
	36	31	7.4	36778	4	US-09-105-537-5			Sequence 5, Appli
	37	31	7.4	38506	3	US-09-320-878-19			Sequence 19, Appl
c	38	31	7.4	44377	2	US-08-804-227C-7			Sequence 7, Appli
c	39	31	7.4	44377	2	US-08-804-198-1			Sequence 1, Appli
c	40	30.8	7.3	8201	1	US-08-253-155A-9			Sequence 9, Appli
c	41	30.6	7.3	1182	1	US-08-241-943-23			Sequence 23, Appl
c	42	30.6	7.3	2327	6	5229279-5			Patent No. 5229279
c	43	30.6	7.3	2327	6	5512669-5			Patent No. 5512669

c	44	30.6	7.3	4984	1	US-08-687-806-1	Sequence 1, Appli
c	45	30.6	7.3	5392	2	US-08-403-852D-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-861-269-4
; Sequence 4, Application US/08861269
; Patent No. 5817494
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,269
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0302 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1197 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT09
; CLONE: 2151473
US-08-861-269-4

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Best Local Similarity	60.7%;	Pred. No. 3.8e-08;		

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 Qy	 346	 gactgctgccaaggacgccattgccaaaggctaataccggtggtgaaggcagacaagctcg	 405
Db	819	AGCCGATGCTGCTGA-GAAAATCAGAAAAGAAAATCCAGTAGTTGTTGGTGAAAAGATCC	877
 Qy	 406	 acaagatctaa	 416
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US-09-134-596-4
; Sequence 4, Application US/09134596
; Patent No. 5922318
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Corley, Neil C.
;   APPLICANT: Lal, Preeti
;   APPLICANT: Shah, Purvi
;   TITLE OF INVENTION:  UBIQUITIN CONJUGATION PROTEINS
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Incyte Pharmaceuticals, Inc.
;     STREET: 3174 Porter Drive
;     CITY: Palo Alto
;     STATE: CA
;     COUNTRY: USA
;     ZIP: 94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/134,596
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/861,269
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Billings, Lucy J.
;     REGISTRATION NUMBER: 36,749
;     REFERENCE/DOCKET NUMBER: PF-0302 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415-855-0555
;     TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:

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;      LENGTH: 1197 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      IMMEDIATE SOURCE:
;      LIBRARY: BRAINOT09
;      CLONE: 2151473
US-09-134-596-4
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Matches 116;  Conservative 0;  Mismatches 74;  Indels 1;  Gaps 1;
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Qy  286 gaacttggtactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacg 345
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Qy  346 gactgctgccaaaggacgccattgccaaagggtctaatccggtggtgaaggcagacaagctcg 405
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Qy  406 acaagatctaa 416
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Db  878 AAAAGATTTGA 888
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RESULT 3
US-09-293-273-4
; Sequence 4, Application US/09293273
; Patent No. 6057112
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,273
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/134,596
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0302 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1197 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT09
; CLONE: 2151473
US-09-293-273-4

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Query Match          14.4%; Score 60.6; DB 3; Length 1197;
Best Local Similarity 60.7%; Pred. No. 3.8e-08;
Matches 116; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

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Qy 286 gaacttgctactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacg 345
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Qy 346 gactgctgccaaaggacgccattgccaaagggttaatccgggtggtgaaggcagacaagctcg 405
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Qy 406 acaagatctaa 416
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Db 878 AAAAGATTTGA 888

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RESULT 4
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria

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; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

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Query Match          8.5%; Score 35.8; DB 1; Length 7218;
Best Local Similarity 1.9%; Pred. No. 0.69;
Matches      7; Conservative 203; Mismatches 156; Indels    0; Gaps      0;

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Qy     116 gtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgtgatgttgcc 175
      : : : : : : : : : : : : : : : : : : : : : : :
Db    1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327

Qy     176 ggacccagcgaggggggtggcggcgatctccaaaggggggaaggtanggccgaaccggtgc 235
      : : : : : : : : : : : : : : : : : : : : : : :
Db    1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267

Qy     236 agcgctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaacttgta 295
      : : : : : : : : : : : : : : : : : : : : : : :
Db    1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207

Qy     296 tgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacggactgctgcc 355

```

```

      : : :       : : :       :: :: : :: : : :: : : : : : :
Db    1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147

Qy     356 aaggacgccattgccaagggctaatccggtggtgaaggcagacaagctcgacaagatcta 415
        ::::: :   :   :   :::::  ::   :: : : ::::: :: : :   :   :::::   :
Db    1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087

Qy     416 agggggg 421
        :::::
Db    1086 RRRRRR 1081
```

```

RESULT      5
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

```

Query Match 8.4%; Score 35.4; DB 4; Length 4411529;
Best Local Similarity 48.8%; Pred. No. 8.1;
Matches 123; Conservative 0; Mismatches 127; Indels 2; Gaps 1;

Qy	8	gcacgcgtccggcaggatcaggccaagctggctgacctctatcgacagcatcgtgaac	67
Db	338607	gccgcgggccccgcggttgacgccggcgccggtatcctcggcgccgcggttgccgat	338666
Qy	68	ggcagcgacgccgtcatggagccggttgctggcagcaacacggtagtagctgttgcc	127
Db	338667	taaccagccgcgctccccgccattggccccggtgccggggcgccggttggtgcggttgcc	338726
Qy	128	caagttgagttgcaaacaatgaacgtgcagcagcccgtgatgttgccggaccagcgag	187
Db	338727	gatcagcggggcgcccggtattcgccaggaagaactcggtgatcggggcg--agcagcggc	338784
Qy	188	ggggtggcggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgctgcagg	247
Db	338785	gaggtggcggcgccctcggcggcggtacgcgcgcaccggaggtcaacgcctgcacg	338844
Qy	248	aaqaggggttqga	259

Db 338845 aactgggcatga 338856

```

RESULT      6
US-08-387-942C-37
; Sequence 37, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
;   APPLICANT:  ERTESVAG, HELGA
;   APPLICANT:  VALLA, SVEIN
;   APPLICANT:  SKJAK-BRAEK, GUDMUND
;   APPLICANT:  LARSEN, BJORN
;   TITLE OF INVENTION:  DNA COMPOUNDS COMPRISING SEQUENCES
;   TITLE OF INVENTION:  ENCODING MANNURONAN C-5-EPIMERASE
;   NUMBER OF SEQUENCES:  52
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BIRCH, STEWART, KOLASCH & BIRCH, LLP
;       STREET:    P.O.BOX 747
;       CITY:      FALLS CHURCH
;       STATE:     VA
;       COUNTRY:   USA
;       ZIP:       22042
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:     IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:      PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/387,942C
;       FILING DATE:       09-MAY-1995
;       CLASSIFICATION:    435
;   ATTORNEY/AGENT INFORMATION:
;       NAME:  MURPHY JR, GERALD M.
;       REGISTRATION NUMBER:  28,977
;       REFERENCE/DOCKET NUMBER:  1809-106P
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-205-8000
;       TELEFAX:   703-205-8050
;   INFORMATION FOR SEQ ID NO:  37:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH:  459 base pairs
;           TYPE:    nucleic acid
;           STRANDEDNESS:  single
;           TOPOLOGY:  linear
;       MOLECULE TYPE:  DNA (genomic)
US-08-387-942C-37

```

Query Match 8.2%; Score 34.6; DB 2; Length 459;
Best Local Similarity 48.5%; Pred. No. 0.56;
Matches 94; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Best Local Similarity 48.5%; Pred. No. 0.56;

Matches 94; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 171 ttgccggagccagcgcgagggggtggcgcgcatctccaaaggggggaaggtanggccgaacc 230
 || ||| || |||| | | | | | | | | | | | | | | | |
 Db 29 TTTCCGGCAGCAGCGCGGCCGAGGAACTGCTCGGCGGGGTCGGCAACGACAGCCTGGACG 88

| | | | | | | | | | | | | | | | | | | | | |

Db 29 TTTCCGGCAGCAGCGCGGCCGAGGAACTGCTCGGCGGGGTCTGGCAACGACAGCCTGGACG 88

Qy 231 ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact 290
 | | | | | | | | | | | | | | | | | |
 Db 89 GCGGCGCCGGCAACGACATCCTCGACGGCGGGGCGGGGCGCGACACCCTGAGTGGCGGCA 148

Qy 291 tgtactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacggactg 350
 | | | | | | | | | | | | | | | | | |
 Db 149 GCGGCGAGCGACATCTTCCGCTTCGGCGGCGCGCTCGACAGCTTCGCAACTACGCCAGCG 208

Qy 351 ctgccaaggacgcc 364
 | | | | | |
 Db 209 GGACGAACGGCACC 222

RESULT 7

US-08-387-942C-1

; Sequence 1, Application US/08387942C

; Patent No. 5939289

; GENERAL INFORMATION:

; APPLICANT: ERTESVAG, HELGA

; APPLICANT: VALLA, SVEIN

; APPLICANT: SKJAK-BRAEK, GUDMUND

; APPLICANT: LARSEN, BJORN

; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES

; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

; STREET: P.O.BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22042

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/387,942C

; FILING DATE: 09-MAY-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURPHY JR, GERALD M.

; REGISTRATION NUMBER: 28,977

; REFERENCE/DOCKET NUMBER: 1809-106P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-205-8000

; TELEFAX: 703-205-8050

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12588 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Azotobacter vinelandii

```

; STRAIN: E
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 290..1951
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2227..6438
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6702..9695
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9973..12588
US-08-387-942C-1

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Query Match 8.2%; Score 34.6; DB 2; Length 12588;
Best Local Similarity 48.5%; Pred. No. 1.8;
Matches 94; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy	171	ttgccggaccacagcgagggggtggcggcgatctccaaaggggggaaggtanggccgaacc	230
Db	9205	TTTCCGGCAGCAGCGCGGCCGAGGAAGTCTCGGCGGGGTCGGCAACGACAGCCTGGACG	9264
Qy	231	ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact	290
Db	9265	GCGGCGCCGGCAACGACATCCTCGACGGCGGGGCGGGGCGCGACACCTGAGTGGCGGCA	9324
Qy	291	tgtactgcgcaactccaccgctactccgacaagcacgactgcaagttcgactaacggactg	350
Db	9325	GCGGCAGCGACATCTTCCGCTTCGGCGGCGCGCTCGACAGCTTCCGCAACTACGCCAGCG	9384
Qy	351	ctgccaaaggacgcc	364
Db	9385	GGACGAACGGCACC	9398

```

RESULT      8
US-09-167-717-3
; Sequence 3, Application US/09167717
; Patent No. 6133014
; GENERAL INFORMATION:
; APPLICANT: MUKOUYAMA, MASAHARU
; APPLICANT: YASUDA, SHINZO
; APPLICANT: KOMATSUZAKI, SATOMI
; TITLE OF INVENTION: MALEATE ISOMERASE GENE
; FILE REFERENCE: PH-555US
; CURRENT APPLICATION NUMBER: US/09/167,717
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: JP 276261/1997
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 3
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)..(750)
US-09-167-717-3

Query Match 8.2%; Score 34.4; DB 3; Length 750;
Best Local Similarity 48.9%; Pred. No. 0.76;
Matches 92; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

```
Qy      14  gtccggcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagc 73
          | ||| || || ||||| ||| | | | | || || | | | | ||| |
Db      511  gcccgtcacgacacggccaacctgccgggcatcgcgccggcatgaaccttgagggcgctc 570

Qy      74  gacgccgtcatggagccggttggtgctggcagcaacacggtagtagctggtgccaagtt 133
          || | || || || | | | | | | | | | | | | | | | |
Db      571  gatgtggtggtgctttcagcctgcgtgcagatgcagtcgctgccggcagtcgccaaggtc 630

Qy     134  gagttgcaaacaatgaacgtgcagcagcccgtgatgttgccggaccagcgagggggtg 193
          ||| ||||| || | | | ||||| | ||| || || | |
Db     631  gaggcgcaaaccggcaaaccggtggtcaccgctgccatgccaccacctacgccatgctc 690

Qy     194  gcggcgat 201
          |||| |
Db     691  aaggcgct 698
```

RESULT 9

US-09-036-987A-1

; Sequence 1, Application US/09036987A

; Patent No. 6143526

; GENERAL INFORMATION:

; APPLICANT: Baltz, Richard H.

; APPLICANT: Broughton, Mary C.

; APPLICANT: Crawford, Kathryn P.

; APPLICANT: Madduri, Krishnamurthy

; APPLICANT: Merlo, Donald J.

; APPLICANT: Treadway, Patti J.

; APPLICANT: Turner, Jan R.

; APPLICANT: Waldron, Clive

; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

; TITLE OF INVENTION: Production

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dow AgroSciences LLC Patent Department

; STREET: 9330 Zionsville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/036,987A

; FILING DATE: 09-MAR-1998


```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1

```

```

Query Match          7.9%; Score 33.2; DB 3; Length 80161;
Best Local Similarity 55.1%; Pred. No. 8.8;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

```

```

Qy      23 gatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgcccgtc 82
          ||||| | | | | | | | | | | | | | | | | | | |
Db 21852 GATCAGGCGCACGCCGATGGCGACCGGATCTACTGCCTCATCCGCGGCAGCGCGGTCAAC 21911

Qy      83 atggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagttgc 140
          | || | | | | | | | | | | | | | | | | |
Db 21912 AACGATGGGGGCGGTGCCGGGCTACCGTTCCGGCGGCGGACGCCAGGCGGAGCTGC 21969

```

```

RESULT 10
US-09-370-700-1
; Sequence 1, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 80161
; TYPE: DNA
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1

```

Query Match 7.9%; Score 33.2; DB 4; Length 80161;
Best Local Similarity 55.1%; Pred. No. 8.8;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

```
Qy      23 gatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgccgtc 82
      ||||| | | | | | | | | | | | | | | | | | |
Db 21852 gatcaggcgcacgccgatggcgaccggatctactgcctcatccgcggcagcgcggtcaac 21911

Qy      83 atggagccggttgttgctggcagcaacacggtagtagctgttgcccaagttgagttgc 140
      | | | | | | | | | | | | | | | | | |
Db 21912 aacgatgggggcggtgccgggtcaccgttcggcgggacgcccaggcgagctgc 21969
```

RESULT 11
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 7.9%; Score 33.2; DB 4; Length 4403765;
Best Local Similarity 47.0%; Pred. No. 26;
Matches 102; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

```
Qy      179 cccagcgaggggggtggcgcgatctccaaaggggggaaggtanggccgaaccggtgcagc 238
      ||| |||| | | | |||| | | | | | | | | | |
Db 1383125 ccccgcgagcggttctcgcgctcaccggtggaccacaatcggcgatctcgagctg 1383184

Qy      239 gcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaacttgactgc 298
      ||| || | | | | | | | | | | | | | | |
Db 1383185 gccccaagaccggcgcggtcaccgacatcaagaagatgacgatctggggcaatcac 1383244

Qy      299 gcactccaccgctactccgacaagcacgactgcaagttcgactaacggactgctgccaag 358
      | | | | | | | | | | | | | | | | | |
Db 1383245 tcggccaccagtagcccgacctgttcacgcggaggtcgccggaaagaacgcggccgaa 1383304
```

Qy 359 gacgccattgccaaagggctaataccgggtggtgaaggca 395
| | | | | | | | | | | | | | | |
Db 1383305 gtggtcaacgaccaggcctggatcgaggatgaattca 1383341

RESULT 12
US-08-981-392-24
; Sequence 24, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; APPLICANT: Henrique, Domingos Manuel Pinto
; APPLICANT: Lewis, Julian Hart
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; 'ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,392
; FILING DATE: 22-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Antler, Adriane M.
; REGISTRATION NUMBER: 32,605
; REFERENCE/DOCKET NUMBER: 7326-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2899 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-981-392-24

Query Match 7.8%; Score 33; DB 4; Length 2899;
Best Local Similarity 35.3%; Pred. No. 3;
Matches 78; Conservative 31; Mismatches 112; Indels 0; Gaps 0;

Qy 147 tgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggcgatctcca 206

```

      |||: |:||| |:| | : :|:| :||| | : |||:| | |:| :| | |
Db  1750 TGARGCTRCAGAARCAACCRGCCYCCASCYAMCCCTGNSGGGGRGAGACRGARACCATGA 1809

Qy   207 aaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttgacttacgg 266
      | : | | | : | | : | | | :||| :||:
Db  1810 ACAACCTRGNCAAYTGCCAGCGYGAGAAGGACRTYTCWGTYAGCATCATYGGGGNYACSC 1869

Qy   267 gattcaactgccggtgtggaacttgactgcgcactccaccgctactccgacaagcacg 326
      |||| | || | ||| : ||| : ||:|:| || ::
Db  1870 ACATCAAGAACACCAACAAGAAGGCGGACTTYCACGGGGACCAYRGNGCCRASAAAGARYR 1929

Qy   327 actgcaagttcgactaacggactgctgccaaggacgccatt 367
      || :||| :| :|| | : :| | | | || | |:
Db  1930 GCTTYAAGGYCCGMTACCCMRNKGTGGACTATAACCTCGTK 1970

```

RESULT 13

US-08-470-058-3

; Sequence 3, Application US/08470058

; Patent No. 5817789

; GENERAL INFORMATION:

; APPLICANT: Heartlein, Michael W.

; APPLICANT: Lemontt, Jeffrey F.

; TITLE OF INVENTION: Chimeric Proteins For Use in Transport

; TITLE OF INVENTION: of a Selected Substance Into Cells

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

; STREET: Two Militia Drive

; CITY: Lexington

; STATE: MA

; COUNTRY: USA

; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,058

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Granahan, Patricia

; REGISTRATION NUMBER: 32,227

; REFERENCE/DOCKET NUMBER: TKT93-01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-861-6240

; TELEFAX: 617-861-9540

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4601 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; MOLECULE TYPE: cDNA to mRNA

US-08-470-058-3

Query Match 7.7%; Score 32.4; DB 1; Length 4601;
Best Local Similarity 58.2%; Pred. No. 5.3;
Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 20 caggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgcc 79
|||| | | | ||||| || ||| ||||| | | || | |||| |
Db 1433 CAGGCCCCCGACGGGCTGGCTGTGGACTGGATCCACAGCAACATCTACTGGACCGACTCT 1492

Qy 80 gtcattggagccggttggttgctggcagcaacacggtagt 117
||| ||| | || || || | || || ||
Db 1493 GTCCTGGGCACTGTCTCTGTTGCGGATACCAAGGGCGT 1530

RESULT 14
US-09-037-188-3
; Sequence 3, Application US/09037188
; Patent No. 6027921
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,188
; FILING DATE: 02-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both

; TOPOLOGY: both
; MOLECULE TYPE: cDNA to mRNA
US-09-037-188-3

Query Match 7.7%; Score 32.4; DB 3; Length 4601;
Best Local Similarity 58.2%; Pred. No. 5.3;
Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 20 caggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgagcc 79
|||| | | | ||||| || || ||||| | | || | |||||
Db 1433 CAGGCCCCCGACGGGCTGGCTGTGGACTGGATCCACAGCAACATCTACTGGACCGACTCT 1492

Qy 80 gtcattggagccggttggtgctggcagcaacacggtagt 117
||| ||| | || || || | || || ||
Db 1493 GTCCTGGGCACTGTCTCTGTTGCGGATACCAAGGGCGT 1530

RESULT 15
US-09-285-310-3

; Sequence 3, Application US/09285310
; Patent No. 6262026
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,310
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 4601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA to mRNA
US-09-285-310-3

Query Match 7.7%; Score 32.4; DB 4; Length 4601;
Best Local Similarity 58.2%; Pred. No. 5.3;
Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 20 caggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgcc 79
|||| | | | ||||| || ||| ||||| | | || | |||||
Db 1433 CAGGCCCCGACGGGCTGGCTGTGGACTGGATCCACAGCAACATCTACTGGACCGACTCT 1492

Qy 80 gtcattggagccggttgctggcagcaacacggtagt 117
||| ||| | || || || | || || ||
Db 1493 GTCCTGGGCACTGTCTCTGTTGCGGATACCAAGGGCGT 1530

Search completed: February 7, 2002, 11:12:10
Job time: 7296 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2002, 08:20:48 ; Search time 4942.22 Seconds
(without alignments)
915.373 Million cell updates/sec

Title: US-09-394-745-6489
Perfect score: 421
Sequence: 1 ggggccagcacgcgtccggc.....ctcgacaagatctaaggggg 421

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*

4: em_estom:*
 5: em_estpl:*
 6: em_estba:*
 7: em_estro:*
 8: em_estov:*
 9: em_htc:*
 10: gb_est1:*
 11: gb_est2:*
 12: gb_htc:*
 13: gb_gss:*
 14: em_gss_fun:*
 15: em_gss_hum:*
 16: em_gss_inv:*
 17: em_gss_pln:*
 18: em_gss_pro:*
 19: em_gss_rod:*
 20: em_gss_vrt:*
 21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

		%							
Result			Query						
No.	Score	Match	Length	DB	ID			Description	
c	1	385.2	91.5	635	11	BG841717		BG841717	MEST24-E1
	2	378.8	90.0	528	10	BE012241		BE012241	945015H01
c	3	378.8	90.0	629	10	AW506899		AW506899	660060H09
	4	367.4	87.3	602	10	AW928018		AW928018	945006F08
	5	362.2	86.0	477	10	BE640589		BE640589	945020B04
	6	351.8	83.6	518	10	BE129631		BE129631	945027C01
	7	348.8	82.9	594	10	AI881804		AI881804	606073E02
	8	331.4	78.7	488	11	BG355155		BG355155	947043D10
c	9	324.8	77.1	482	10	BE510926		BE510926	946056E05
	10	312.8	74.3	567	10	AW927909		AW927909	945010H04
c	11	290.6	69.0	643	10	AI977903		AI977903	496035D05
c	12	290	68.9	514	10	AW061851		AW061851	687007F12
	13	287.4	68.3	527	10	AI649645		AI649645	486077B07
c	14	276.8	65.7	599	10	BE129734		BE129734	946003G07
	15	264.2	62.8	660	11	W99253		W99253	EST01 Gluco
	16	263.8	62.7	598	10	AW924551		AW924551	WS1_70_F0
	17	260.6	61.9	582	10	BE361054		BE361054	DG1_69_E0
	18	259.6	61.7	595	11	BI246082		BI246082	IP1_68_E1
	19	259.4	61.6	479	11	BE918267		BE918267	OV1_1_C02
	20	258	61.3	549	10	AW231809		AW231809	687042A08
	21	256.6	61.0	547	11	BE918046		BE918046	OV1_1_C02
	22	255.4	60.7	586	10	BE363253		BE363253	WS1_61_F0
c	23	254.4	60.4	608	10	BE055927		BE055927	945020B03
c	24	254.2	60.4	612	10	AI734759		AI734759	606036A08
	25	253.4	60.2	662	11	BG932962		BG932962	DG1_69_E0
c	26	247.2	58.7	594	10	AI622011		AI622011	486031B05
c	27	245	58.2	651	10	AI861117		AI861117	603012D01
	28	244	58.0	555	10	AW680999		AW680999	WS1_9_D08
	29	243.6	57.9	662	11	BG464005		BG464005	EM1_52_E0

	30	241.6	57.4	649	11	BG465281	BG465281	EM1_74_C1
c	31	241.4	57.3	582	10	AI691879	AI691879	606011G11
c	32	238	56.5	327	10	AW433452	AW433452	707069H08
	33	234.8	55.8	491	10	AW924565	AW924565	WS1_70_F0
	34	232.4	55.2	473	10	BE051771	BE051771	za87h06.g
c	35	230.6	54.8	467	10	AI861162	AI861162	603017B08
	36	221	52.5	231	10	BE640588	BE640588	945020B03
	37	219	52.0	538	11	BG313898	BG313898	WHE2066_D
	38	217	51.5	525	11	BG356205	BG356205	EM1_22_G0
	39	216.2	51.4	620	11	BF473074	BF473074	WHE0925_D
	40	216.2	51.4	693	10	BE585592	BE585592	EST#5PSP6
	41	215	51.1	571	10	BE420025	BE420025	WWS02.C8R
	42	213.6	50.7	260	10	BE056027	BE056027	945017E04
c	43	211.6	50.3	830	10	BE705552	BE705552	Sc01_03a0
	44	211	50.1	664	10	BE431005	BE431005	SUN010.CO
c	45	210.8	50.1	715	10	BE705540	BE705540	Sc01_02h0

ALIGNMENTS

RESULT 1
BG841717/c

LOCUS BG841717 635 bp mRNA EST 29-MAY-2001

DEFINITION MEST24-E10.T3 ISUM4-TN Zea mays cDNA clone MEST24-E10 3', mRNA sequence.

ACCESSION BG841717

VERSION BG841717.2 GI:14244031

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 635)

AUTHORS Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.

TITLE Expressed Sequence Tags from B73 Maize Seedlings and Silks

JOURNAL Unpublished (2001)

COMMENT On May 25, 2001 this sequence version replaced gi:14208039.
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

PCR Primers
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
source Location/Qualifiers
1. .635
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST24-E10"
/clone_lib="ISUM4-TN"

/tissue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AACTGGAAGAATTCGCGGCCGAGGAATTTTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT7T3PAC vector. The library
then went through one round of normalization to CoT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT 132 a 190 c 166 g 147 t
ORIGIN

Query Match 91.5%; Score 385.2; DB 11; Length 635;
Best Local Similarity 98.8%; Pred. No. 4e-82;
Matches 398; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy      19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
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Db      630 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 571

Qy      79 cgtcatggagccggttggtgctggcagcaacacggtagtagctggtgcccagttgagtt 138
          |||
Db      570 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTTGAGTT 511

Qy     139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgagggggtggcggc 198
          |||
Db      510 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 451

Qy     199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttg 258
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Db      450 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 391

Qy     259 acttacgggattcaactgccggtgtgggaactgtactgcgcactccaccgctactccga 318
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Db      390 ACTTACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCACTCCACCGCTACTCCGA 331

Qy     319 caagcacgactgcaagttcgactaacggactgctgccaaaggacgccattgccaaagggcta 378
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Db      330 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 272

Qy     379 atccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
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Db      271 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 229

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RESULT 2
BE012241
LOCUS BE012241 528 bp mRNA EST 06-JUN-2000
DEFINITION 945015H01.Y1 945 - Mixed adult tissues from Walbot lab, same as 707

(SK) Zea mays cDNA, mRNA sequence.

ACCESSION BE012241

VERSION BE012241.1 GI:8273149

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 528)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 945015 row: H column: 01.

FEATURES Location/Qualifiers

source 1..528
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="945 - Mixed adult tissues from Walbot lab,
same as 707 (SK)"
/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."

BASE COUNT 120 a 146 c 176 g 86 t

ORIGIN

Query Match 90.0%; Score 378.8; DB 10; Length 528;
Best Local Similarity 97.8%; Pred. No. 1.3e-80;
Matches 394; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
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Db 127 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 186

Qy 79 cgtcatggagccggttgctggcagcaacacggtagtagctgttgcccaagttgagtt 138
|||||

Db 187 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 246

Qy 139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggaaccagcgaggggggtggcggc 198
|||||

Db 247 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGAACCCAGCGAGGGGGTGGCGGC 306

Qy 199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgctgcaggaagagggttgg 258
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 Db 307 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 366
 Qy 259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
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 Db 367 GCTCACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCGCTCCACCGCTACTCCGA 426
 Qy 319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagggcta 378
 |||
 Db 427 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 485
 Qy 379 atccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
 |||
 Db 486 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 528

RESULT 3
 AW506899/c
 LOCUS AW506899 629 bp mRNA EST 03-MAR-2000
 DEFINITION 660060H09.x1 660 - Mixed stages of anther and pollen Zea mays cDNA,
 mRNA sequence.
 ACCESSION AW506899
 VERSION AW506899.1 GI:7145418
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 629)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 660060 row: H column: 09.
 FEATURES Location/Qualifiers
 source 1. .629
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="660 - Mixed stages of anther and pollen"
 /tissue_type="whole premieotic anthers to pollen shed"
 /dev_stage="premieotic anthers to pollen shed"
 /lab_host="XL0LR"
 /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
 Site_2: XhoI; Anther and pollen cDNA library.
 Directionally sequenced with 5' end at the EcoRI site.
 Created by Amie Franklin."

BASE COUNT 137 a 193 c 171 g 128 t
ORIGIN

Query Match 90.0%; Score 378.8; DB 10; Length 629;
Best Local Similarity 97.8%; Pred. No. 1.4e-80;
Matches 394; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy     19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
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Db   622 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 563

Qy     79 cgtcatggagccggttggtgctggcagcaacacggtagtagctggtgcccagttgagtt 138
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Db   562 CGTCATGGAGCCGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 503

Qy   139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggc 198
      |||
Db   502 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 443

Qy   199 gatctccaaaggggggaaggtanggccgaaccgggtgcagcgccctgcaggaagaggggttg 258
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Db   442 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 383

Qy   259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
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Db   382 GCTCACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCGCTCCACCGCTACTCCGA 323

Qy   319 caagcacgactgcaagttcgactaacggactgctgccaaaggacgccattgccaaagggcta 378
      |||
Db   322 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 264

Qy   379 atccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
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Db   263 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 221
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RESULT 4

AW928018

LOCUS AW928018 602 bp mRNA EST 30-MAY-2000

DEFINITION 945006F08.Y1 945 - Mixed adult tissues from Walbot lab, same as 707
(SK) Zea mays cDNA, mRNA sequence.

ACCESSION AW928018

VERSION AW928018.1 GI:8103377

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 602)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences

Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945006 row: F column: 08.

FEATURES Location/Qualifiers
 source 1. .602
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="945 - Mixed adult tissues from Walbot lab,
 same as 707 (SK)"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /note="Organ: tassel, kernal, silk, husk, root, leaf;
 Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
 differentiated maize tissues from an active Mutator plant.
 Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
 root, leaf). Unidirectionally cloned. New library number
 given to library 707 for additional sequencing."
 BASE COUNT 134 a 176 c 191 g 101 t
 ORIGIN

Query Match 87.3%; Score 367.4; DB:10; Length 602;
 Best Local Similarity 97.9%; Pred. No. 7e-78;
 Matches 382; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Qy      19  gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
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Db      214 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 273

Qy      79  cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccaggttgagtt 138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 333

Qy     139  gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggc 198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     334  GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 393

Qy     199  gatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttg 258
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     394  GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 453

Qy     259  acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
          || ||||||||||||||||||||||||||||||||||||||||||||||||
Db     454  GCTCACGGGATTCAACTGCCGGTGTGGGAACCTGTACTGCGCGCTCCACCGCTACTCCGA 513

Qy     319  caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagggcta 378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514  CAAGCACGACTGCAAGTTGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 572

Qy     379  atccggtggtgaaggcagacaagctcgaca 408
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Db     573  ATCCGGTGGTGAAGGCAGACAAGCTCGACA 602
  
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RESULT 5
 BE640589
 LOCUS BE640589 477 bp mRNA EST 30-AUG-2000
 DEFINITION 945020B04.X1 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence..
 ACCESSION BE640589
 VERSION BE640589.1 GI:9954021
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 477)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945020 row: B column: 04.
 FEATURES Location/Qualifiers
 source 1. .477
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /note="Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."
 BASE COUNT 109 a 130 c 151 g 87 t
 ORIGIN

Query Match 86.0%; Score 362.2; DB 10; Length 477;
 Best Local Similarity 96.2%; Pred. No. 1.2e-76;
 Matches 381; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
 |||||||||||||||||||||||||||||||||||||||||||||
 Db 83 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAATCTTTTCGACGC 142
 Qy 79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccaggttgagtt 138

```

      |||
Db    143 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGGTGCCCAAGTCGAGTT 202
      |||
Qy    139 gcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggc 198
      |||
Db    203 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 262
      |||
Qy    199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttg 258
      |||
Db    263 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 322
      |||
Qy    259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
      |||
Db    323 GCTCACGGGATTCAACTGCCGGTGTGGGAACCTGTACTGCGCGCTCCACCGCTACTCCGA 382
      |||
Qy    319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaaagggcta 378
      |||
Db    383 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTA 441
      |||
Qy    379 atccggtggtgaaggcagacaagctcgacaagatct 414
      |||
Db    442 ATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCT 477

```

RESULT 6

BE129631

LOCUS BE129631 518 bp mRNA EST 21-JUN-2000

DEFINITION 945027C01.X2 945 - Mixed adult tissues from Walbot lab, same as 707 (SK) Zea mays cDNA, mRNA sequence.

ACCESSION BE129631

VERSION BE129631.1 GI:8576994

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 518)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
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Email: walbot@stanford.edu
Plate: 945027 row: C column: 01.

FEATURES

source

Location/Qualifiers

1. .518

/organism="Zea mays"

/cultivar="W23"

/db_xref="taxon:4577"

/clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"


```

/tissue_type="tassel, kernal, silk, husk, root, leaf"
/dev_stage="fully-grown"
/lab_host="DH10B"
/note="Organ: tassel, kernal, silk, husk, root, leaf;
Vector: pGAD10; Site_1: EcoRI; cDNA library from fully
differentiated maize tissues from an active Mutator plant.
Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk,
root, leaf). Unidirectionally cloned. New library number
given to library 707 for additional sequencing."

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BASE COUNT      105 a      141 c      169 g      103 t
ORIGIN

```

```

Query Match          83.6%;  Score 351.8;  DB 10;  Length 518;
Best Local Similarity 97.6%;  Pred. No. 3.6e-74;
Matches 367;  Conservative 0;  Mismatches 8;  Indels 1;  Gaps 1;

```

```

Qy      46 ctctatcgacagcatcgtgaacggcagcgacgccgtcatggagccggttggtgctggcag 105
      |||
Db       1 CTCTATCGACAGCATCGTGAACGGCAGCGACGCCGTCATGGAGCCGTTGTTGCTGGCAG 60

Qy     106 caacacggtagtagctggttgcccaagttgagttgcaaacaatgaacgtgcagcagcccg 165
      |||
Db      61 CAACACGGTAGTAGCTGTTGCCCAAGTCGAGTTGCAAACAATGAACGTGCAGCAGCCCGC 120

Qy     166 tgatggttgccggacccagcgaggggggtggcgcgatctccaaaggggggaaggtangggcc 225
      |||
Db     121 TGATGTTGCCGGACCCAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCC 180

Qy     226 gaaccggtgcagcgccctgcaggaagaggggttgacttacgggattcaactgccggtgtgg 285
      |||
Db     181 GAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGGGCTCACGGGATTCAACTGCCGGTGTGG 240

Qy     286 gaacttgtagtgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacg 345
      |||
Db     241 GAACTTGTACTGCGCGCTCCACCGCTACTCCGACAAGCACGACTGCAAGTTGCGACTACCG 300

Qy     346 gactgctgccaaaggacgccattgccaaagggctaataccggtggtgaaggcagacaagctcg 405
      |||
Db     301 GACTGCTGCCAGGGACGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCG 359

Qy     406 acaagatctaaggggg 421
      |||
Db     360 ACAAGATCTAGGGGGG 375

```

```

RESULT      7
AI881804
LOCUS      AI881804      594 bp      mRNA      EST      02-FEB-2000
DEFINITION 606073E02.y1 606 - Ear tissue cDNA library from Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION  AI881804
VERSION    AI881804.1  GI:5566893
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 594)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
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 Plate: 606073 row: E column: 02.

FEATURES Location/Qualifiers

source 1. .594
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="606 - Ear tissue cDNA library from Schmidt
 lab"
 /tissue_type="mixed"
 /dev_stage="ear length from 0.5 cm - 2.0 cm"
 /lab_host="XLRLR (Stratagene)"
 /note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcoRI
 ; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
 lab"

BASE COUNT 132 a 173 c 191 g 98 t

ORIGIN

Query Match 82.9%; Score 348.8; DB 10; Length 594;
 Best Local Similarity 95.2%; Pred. No. 1.9e-73;
 Matches 359; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgatgaacggcagcgacgc 78
 |||

Db 215 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 274

Qy 79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138
 |||

Db 275 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTT 334

Qy 139 gcaaacaatgaacgtgcagcagcccgctgatggtgcccggacccagcgagggggtggcggc 198
 |||

Db 335 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 394

Qy 199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgccctgcaggaagaggggttg 258
 |||

Db 395 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 454

Qy 259 acttacgggattcaactgccggtgtgggaacttgtagtgcgcactccaccgctactccga 318
 |||

Db 455 GCTCACGGGATTCAACTGCCGGTGTGGGAAGTTGTACTGCGCGCTCCACCGCTACTCCGA 514

Qy 319 caagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaagggcta 378

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      |||
Db    515 CAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAAGGCTAA 574
      |||
Qy    379 atccggtggtgaaggca 395
      |||
Db    575 TCCGGGGGAAGCAGACA 591

```

Qy 19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
 |||
 Db 155 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 214

Qy 79 cgtcatggagccggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138
 |||
 Db 215 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTTGAGTT 274

Qy 139 gcaaacaatgaacgtgcagcagcccgtgatgttgccggacccagcgagggggtggcggc 198
 |||
 Db 275 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 334

Qy 199 gatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagagggttg 258
 |||
 Db 335 GATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 394

Qy 259 acttacgggattcaactgccggtgtgggaacttgactgcgactccaccgctactccga 318
 |||
 Db 395 ACTTACGGGATTCAACTGCCGGTGTGGGAATTGTACTGCGCACTCCACCGCTACTCCGA 454

Qy 319 caagcacgactgcaagttcgactaacggactgct 352
 |||
 Db 455 CAAGCACGACTGCAAGTTCGACTACCGGACTGCT 488

RESULT 9

BE510926/c

LOCUS BE510926 482 bp mRNA EST 07-AUG-2000

DEFINITION 946056E05.x1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BE510926

VERSION BE510926.1 GI:9732174

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 482)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
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 Email: walbot@stanford.edu
 Plate: 946056 row: E column: 05.

FEATURES

source

Location/Qualifiers

1. .482

/organism="Zea mays"

/cultivar="OH43"

/db_xref="taxon:4577"

/clone_lib="946 - tassel primordium prepared by Schmidt

lab"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to
 inflorescence development"
 /lab_host="XL0LR"
 /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI;
 Site_2: XhoI; George Chuck dissected immature tassels
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA
 library in HybriZAP. Sample insert size range was 350 bp
 to 3 Kb with a 1 Kb average."

BASE COUNT 98 a 158 c 131 g 95 t
 ORIGIN

Query Match 77.1%; Score 324.8; DB 10; Length 482;
 Best Local Similarity 97.4%; Pred. No. 1e-67;
 Matches 340; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

```

Qy      73 cgacgccgtcatggagccggttggtgctggcagcaacacggtagtagctggtgccccagt 132
      |||
Db     482 CGACGCCGTCATGGAGCCGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGT 423

Qy     133 tgagttgcaaacaatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggt 192
      |||
Db     422 CGAGTTGCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGT 363

Qy     193 ggcggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagag 252
      |||
Db     362 GCGGCGATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAG 303

Qy     253 ggttggaacttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgcta 312
      |||
Db     302 GGTGGGCTCACGGGATTCAACTGCCGGTGTGGGAAC TTGACTGCGCGCTCCACCGCTA 243

Qy     313 ctccgacaagcacgactgcaagttcgactaacggactgctgccaaggacgccattgccaa 372
      |||
Db     242 CTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA 183

Qy     373 gggctaatccggtggtgaaggcagacaagctcgacaagatctaaggggg 421
      |||
Db     182 -GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 135
  
```

RESULT 10
 AW927909
 LOCUS AW927909 567 bp mRNA EST 30-MAY-2000
 DEFINITION 945010H04.Y1 945 - Mixed adult tissues from Walbot lab, same as 707
 (SK) Zea mays cDNA, mRNA sequence.
 ACCESSION AW927909
 VERSION AW927909.1 GI:8103259
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 567)

AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 945010 row: H column: 04.

FEATURES Location/Qualifiers
 source 1. .567
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="945 - Mixed adult tissues from Walbot lab, same as 707 (SK)"
 /tissue_type="tassel, kernal, silk, husk, root, leaf"
 /dev_stage="fully-grown"
 /lab_host="DH10B"
 /note="Organ: tassel, kernal, silk, husk, root, leaf; Vector: pGAD10; Site_1: EcoRI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing."

BASE COUNT 113 a 147 c 177 g 130 t
 ORIGIN

Query Match 74.3%; Score 312.8; DB 10; Length 567;
 Best Local Similarity 97.3%; Pred. No. 7.4e-65;
 Matches 328; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

```

Qy      85 ggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagttgcaaac 144
      |||
Db      1 GGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTCGAGTTGCAAAC 60

Qy     145 aatgaacgtgcagcagcccgctgatgttgccggacccagcgaggggggtggcggcgatctc 204
      |||
Db     61 AATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGCGATCTC 120

Qy     205 caaaggggggaaggtanggccgaaccggtgcagcgcctgcaggaagaggggttgacttac 264
      |||
Db     121 CAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGGGCTCAC 180

Qy     265 gggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccgacaagca 324
      |||
Db     181 GGGATTCAACTGCCGGTGTGGGAACCTGTACTGCGCGCTCCACCGCTACTCCGACAAGCA 240

Qy     325 cgactgcaagttcgactaacggactgctgccaaggacgccattgccagggttaaatccgg 384
      |||
Db     241 CGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGACGCCATTGCCAA-GGCTAATCCGG 299

Qy     385 tggatgaaggcagacaagctcgacaagatctaaggggg 421
  
```

Db 300 TGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGGG 336

RESULT 11
AI977903/c
LOCUS AI977903 643 bp mRNA EST 27-AUG-1999
DEFINITION 496035D05.x1 496 - stressed shoot cDNA library from Wang/Bohnert
lab Zea mays cDNA, mRNA sequence.
ACCESSION AI977903
VERSION AI977903.1 GI:5791111
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 643)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 496035 row: D column: 05.
FEATURES Location/Qualifiers
source 1. .643
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="496 - stressed shoot cDNA library from
Wang/Bohnert lab"
/tissue_type="seedling"
/dev_stage="salt stress"
/lab_host="E.coli XL Gold"
/note="Organ: shoot; Vector: pBluescriptII SK(+) XR;
Wang/Bohnert"
BASE COUNT 164 a 192 c 159 g 128 t
ORIGIN

Query Match 69.0%; Score 290.6; DB 10; Length 643;
Best Local Similarity 98.1%; Pred. No. 1.5e-59;
Matches 304; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 112 ggtagtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagccccgctgatgt 171
|||||
Db 643 GGTAGTAGCTGTTGCCCAAGTTGAGTTGCAACCAATGAACGTGCAGCAGCCCCGCTGATGT 584
Qy 172 tgccggacccagcaggggggtggcggcgatctccaaaggggggaagggtanggccgaaccg 231
|||||
Db 583 TGCCGGACCCAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCCGAACCG 524

Qy 232 gtgcagcgctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaactt 291
 |||
 Db 523 GTGCAGCGCCTGCAGGAAGAGGGTTGGACTTACGGGATTCAACTGCCGGTGTGGGAACCTT 464

Qy 292 gtactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacggactgc 351
 |||
 Db 463 GTACTGCGCACTCCACCGCTACTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTGC 404

Qy 352 tgccaaggacgccattgccaagggctaataccggtggtgaaggcagacaagctcgacaaga 411
 |||
 Db 403 TGCCAGGGACGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAGA 345

Qy 412 tctaaggggg 421
 |||
 Db 344 TCTAGGGGGG 335

RESULT 12

AW061851/c

LOCUS AW061851 514 bp mRNA EST 30-MAR-2000

DEFINITION 687007F12.x1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.

ACCESSION AW061851

VERSION AW061851.1 GI:6012414

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 514)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 687007 row: F column: 12.

FEATURES Location/Qualifiers

source 1. .514
 /organism="Zea mays"
 /cultivar="Illinois High Oil"
 /db_xref="taxon:4577"
 /clone_lib="687 - Early embryo from Delaware"
 /tissue_type="embryo"
 /dev_stage="14, 21, 28, and 35 days after pollination"
 /lab_host="E. coli SOLR"
 /note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI
 ; Site_2: EcoRI; Library was prepared by Statagene using
 the Uni-ZAP XR system (Stratagene BN937328-12). Clones
 were picked by a Q-bot after blue/white selection

(ampicillin resistance - use 100 micrograms/microliter).
 Developed from a pool of equal amounts of RNA from
 developing embryos sampled at 14, 21, 28 and 35 days after
 pollination of the Illinois High Oil Maize Strain Cycle
 90. This closed strain has been selected for high oil
 concentration for 90 generations and originates from the
 1890s era open pollinated variety Burr's White"

BASE COUNT 116 a 156 c 138 g 104 t
 ORIGIN

Query Match 68.9%; Score 290; DB 10; Length 514;
 Best Local Similarity 97.7%; Pred. No. 2e-59;
 Matches 304; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

```

Qy   111  cggtagtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgctgatg 170
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   513  CGGTAGTAGCTGTTGCCCAAGTTGAGTTGCAAACAATGAACGTGCAGCAGCCCGCTGATG 454

Qy   171  ttgccggacccagcagaggggggtggcggcgatctccaaaggggggaaggtanggccgaacc 230
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   453  TTGCCGACCCAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGCCCGAACC 394

Qy   231  ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact 290
      |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   393  GGTGCAGCGCCTGCAGGAAGAGGGTTGGACTTACGGGATTCAACTGCCGGTGTGGGA ACT 334

Qy   291  tgtactgcgcactccaccgctactccgacaagcagcactgcaagttcgactaacggactg 350
      |||||||||||||||||||||||||||||||||||||||||||||||||
Db   333  TGTACTGCGCACTCCACCGCTACTCCGACAAGCAGCACTGCAAGTTCGACTACCGGTCTG 274

Qy   351  ctgccaaggacgccattgccaaagggctaataccggtggtgaaggcagacaagctcgacaag 410
      ||||||| ||||||||||||||||||| |||||||||||||||||||
Db   273  CTGCCAGGGACGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAG 215

Qy   411  atctaagggggg 421
      ||||| |||||
Db   214  ATCTAGGGGGG 204
  
```

RESULT 13
 AI649645
 LOCUS AI649645 527 bp mRNA EST 30-APR-1999
 DEFINITION 486077B07.y1 486 - leaf primordia cDNA library from Hake lab Zea
 mays cDNA, mRNA sequence.
 ACCESSION AI649645
 VERSION AI649645.1 GI:4730479
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 527)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 University

JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 486077 row: B column: 07.

FEATURES Location/Qualifiers
 source 1. .527
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone_lib="486 - leaf primordia cDNA library from Hake
 lab"
 /tissue_type="leaf primordia"
 /dev_stage="P7-P11 leaf"
 /lab_host="E.coli XL1-Blue MFR"
 /note="Organ: shoot; Vector: Lambda zap; Hake lab cDNA
 library."

BASE COUNT 117 a 151 c 169 g 90 t
 ORIGIN

Query Match 68.3%; Score 287.4; DB 10; Length 527;
 Best Local Similarity 99.0%; Pred. No. 8.5e-59;
 Matches 299; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      19 gcaggatcaggccaagctggctgcctcctctatcgacagcatcgtgaacggcagcgacgc 78
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Db      226 GCAGGATCAGGCCAAGCTGGCTGCCTCCTCTATCGACAGCATCGTGAACGGCAGCGACGC 285

Qy      79 cgtcatggagccggttggttgctggcagcaacacggtagtagctggtgcccagttgagtt 138
      |||
Db      286 CGTCATGGAGCCGGTTGTTGCTGGCAGCAACACGGTAGTAGCTGTTGCCCAAGTTGAGTT 345

Qy      139 gcaaacaatgaacgtgcagcagcccgctgatggttgccggacccagcgaggggggtggcggc 198
      |||
Db      346 GCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACCCAGCGAGGGGGTGGCGGC 405

Qy      199 gatctccaaaggggggaaggtangggccgaaccggtgcagcgccctgcaggaagaggggttg 258
      |||
Db      406 GATCTCCAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGCCTGCAGGAAGAGGGTTGG 465

Qy      259 acttacgggattcaactgccggtgtgggaacttgactgcgcactccaccgctactccga 318
      |||
Db      466 ACTTACGGGATTCAACTGCCGG-GGGGAACTGTACTGCGCACTCCACCGCTACTCCGA 524

Qy      319 ca 320
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Db      525 CA 526
  
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RESULT 14
 BE129734/c
 LOCUS BE129734 599 bp mRNA EST 21-JUN-2000

DEFINITION 946003G07.X1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.
 ACCESSION BE129734
 VERSION BE129734.1 GI:8577097
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 599)
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
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 Email: walbot@stanford.edu
 Plate: 946003 row: G column: 07.
 FEATURES Location/Qualifiers
 source 1..599
 /organism="Zea mays"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /clone_lib="946 - tassel primordium prepared by Schmidt lab"
 /tissue_type="tassels"
 /dev_stage="just after the transition from vegetative to inflorescence development"
 /lab_host="XL0LR"
 /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
 BASE COUNT 149 a 182 c 152 g 116 t
 ORIGIN

Query Match 65.7%; Score 276.8; DB 10; Length 599;
 Best Local Similarity 97.0%; Pred. No. 2.9e-56;
 Matches 292; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy 121 tgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgctgatgttgccggacc 180
    |||
Db 599 TGTTGCCCAAGTCGAGTTGCAAACAATGAACGTGCAGCAGCCCGCTGATGTTGCCGGACC 540

Qy 181 cagcgaggggggtggcggcgatctccaaaggggggaaggtanggccgaaccggtgcagcgc 240
    |||
Db 539 CAGCGAGGGGGTGGCGGCGATCTCCAAAGGGGGGAAGGTAGGGCCGAACCGGTGCAGCGC 480

Qy 241 ctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaacttgactgcgc 300
    |||
  
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Db      479 CTGCAGGAAGAGGGTTGGGCTCACGGGATTCAACTGCCGGTGTGGGAACCTGTACTGCGC 420
Qy      301 actccaccgctactccgacaagcacgactgcaagttcgactaacggactgctgccaagga 360
        |||
Db      419 GCTCCACCGCTACTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTGCTGCCAGGGA 360
Qy      361 cgccattgccaaggggctaatccggtggtgaaggcagacaagctcgacaagatctaagggg 420
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Db      359 CGCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAGATCTAGGGGG 301
Qy      421 g 421
        |
Db      300 G 300

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RESULT 15

W99253

LOCUS W99253 660 bp mRNA EST 17-JUL-1996

DEFINITION EST01 Glucose-starved maize root tip cDNA library Zea mays cDNA clone MZ2B1 3' similar to Phaseolus vulgaris PVPR3, mRNA sequence.

ACCESSION W99253

VERSION W99253.1 GI:1432180

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 660)

AUTHORS Couee, I. and Chevalier, C.

TITLE Maize root cDNAs

JOURNAL Unpublished (1996)

COMMENT Contact: Couee I

Station d'amelioration des arbres forestiers

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F-45160 Ardon, France

Fax: 33-38417879

Email: couee@orleans.inra.fr

Similarity determined by BLASTX.

FEATURES Location/Qualifiers

source 1. .660

/organism="Zea mays"

/cultivar="DEA"

/db_xref="taxon:4577"

/clone="MZ2B1"

/clone_lib="Glucose-starved maize root tip cDNA library"

/tissue_type="3-mm-long tip"

/note="Organ: Primary root; Vector: Lambda ZAPII; cDNA library from poly(A)+ mRNA of 24-h glucose-starved maize root tips, as described in Chevalier, C., Bourgeois, E., Pradet, A., Raymond, P. (1995) Plant Molecular Biology Volume 28 Pages 473-485"

BASE COUNT 142 a 165 c 196 g 154 t 3 others

ORIGIN

Query Match 62.8%; Score 264.2; DB 11; Length 660;

Best Local Similarity 95.1%; Pred. No. 3e-53;
Matches 292; Conservative 0; Mismatches 12; Indels 3; Gaps 2;

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Qy 113 gtagtagctgttgcccaagttgagttgcaaacaatgaacgtgcagcagcccgctgatgtt 172
      |||
Db 1 GTAGTAGCTGTTGCCCAAGTCGAGTTGCAAACAATGAACGTGCAGCAGCCCGCNGATGTT 60

Qy 173 gccggacccagcgaggggg--tggcggcgatctccaaaggggggaaggtanggccgaacc 230
      |||
Db 61 GCCGGACCCAGCGAGGGGGGTTGGCGGCGATCTCCAAAGGGGGAAGGTAGGGCCGAACC 120

Qy 231 ggtgcagcgcctgcaggaagaggggttgacttacgggattcaactgccggtgtgggaact 290
      |||
Db 121 GGTGCAGCGCCTGCAGGAAGAGGGTTGGGCTCACGGGATTCAACTGCCGGTGTGGGAAC 180

Qy 291 tgtactgcgcactccaccgctactccgacaagcacgactgcaagttcgactaacggactg 350
      |||
Db 181 TGTACTGCNCCCTCCACCGCTACTCCGACAAGCACGACTGCAAGTTCGACTACCGGACTG 240

Qy 351 ctgccaaggacgccattgccaaagggctaatccggtggtgaaggcagacaagctcgacaag 410
      |||
Db 241 CTGCCAGGGATNCCATTGCCAA-GGCTAATCCGGTGGTGAAGGCAGACAAGCTCGACAAG 299

Qy 411 atctaag 417
      |||
Db 300 ATCTAGG 306
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